SEQUENCE LISTING

<110> Junghans, Richard P.

<120> Chimeric Effector Cell Receptors Against Carcinoembryonic Antigen

<130> 002

<140> 10/006,771
<141> 2001-12-10

<150> 60/250,090
<151> 2000-11-30

<160> 6

<170> PatentIn version 3.1

<210> 1
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<213> Homo sapiens

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<222> (2428)..(3759)
<223> Chimeric IgTCR sequence contained in retroviral vector. Retrovir
       al vector sequence (non-coding regions) are incidental to the inv
       ention. The translated (coding region) is relevant to the invent
       ion. (pertinent to Figure 3.)

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agagtcattt ctttggtagg aaagtacatt ggcacgtaaa ggagcccaaa gcaatctgtg   180

gaaagcccag gctgggagcc cagcagtttg catcccctcc tggcgtgtac ctaagggttt   240

cttaattgtg tggtttctaa atcttccaga gggtttgtct cattcacttc cacttcggtg   300

cacaatactt ggacgcggat ttactgtctt agcatctatc ggtggccctt cgattgaggc   360

tgaacctgag gcccacttct tcagcttgtt aaggagagca caagcaccag aagaggctga   420

cccggcagac ctgtggggcat ttttaacaag ggcctcctgg gtctgtggga ggcaggctta   480

cataaggtgc aaattagaaa tataaataat aagcccatat caatttgtca tctttttta   540

agctcaagtt ttgaaagacc ccacctgtag gtttggcaag ctagcttaag taacgccatt   600

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cctcaaagta gacggcatcg cagcttggat acacgccgcc cacgtgaagg ctgccgaccc    2400

cgggggtgga ccatcctcta gactgcc atg gga tgg agc tgt atc atc ctc ttc    2454
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                                   1               5
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ttg gta gca aca gct aca ggt gtc cac tcc gac atc cag ctg acc cag    2502
Leu Val Ala Thr Ala Thr Gly Val His Ser Asp Ile Gln Leu Thr Gln
 10              15              20              25
```

```
agc cca agc agc ctg agc gcc agc gtg ggt gac aga gtg acc atc acc    2550
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
                 30              35              40
```

```
tgt aag gcc agt cag gat gtg ggt act tct gta gct tgg tac cag cag    2598
Cys Lys Ala Ser Gln Asp Val Gly Thr Ser Val Ala Trp Tyr Gln Gln
             45              50              55
```

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aag cca ggt aag gct cca aag ctg ctg atc tac tgg aca tcc acc cgg    2646
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Trp Thr Ser Thr Arg
         60              65              70
```

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cac act ggt gtg cca agc aga ttc agc ggt agc ggt agc ggt acc gac    2694
His Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
     75              80              85
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ttc acc ttc acc atc agc agc ctc cag cca gag gac atc gcc acc tac    2742
Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr
 90              95              100             105
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tac tgc cag caa tat agc ctc tat cgg tcg ttc ggc caa ggg acc aag    2790
Tyr Cys Gln Gln Tyr Ser Leu Tyr Arg Ser Phe Gly Gln Gly Thr Lys
             110             115             120
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gtg gaa atc aaa cga ggt ggc tca gga tcg ggt gga tcc ggc tct ggt    2838
Val Glu Ile Lys Arg Gly Gly Ser Gly Ser Gly Gly Ser Gly Ser Gly
            125             130             135

ggc tca gga tcg gag gtc caa ctg gtg gag agc ggt gga ggt gtt gtg    2886
Gly Ser Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val
            140             145             150

caa cct ggc cgg tcc ctg cgc ctg tcc tgc tcc gca tct ggc ttc gat    2934
Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Asp
            155             160             165

ttc acc aca tat tgg atg agt tgg gtg aga cag gca cct gga aaa ggt    2982
Phe Thr Thr Tyr Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly
170             175             180             185

ctt gag tgg att gga gaa att cat cca gat agc agt acg att aac tat    3030
Leu Glu Trp Ile Gly Glu Ile His Pro Asp Ser Ser Thr Ile Asn Tyr
                190             195             200

gcg ccg tct cta aag gat aga ttt aca ata tcg cga gac aac gcc aag    3078
Ala Pro Ser Leu Lys Asp Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys
            205             210             215

aac aca ttg ttc ctg caa atg gac agc ctg aga ccc gaa gac acc ggg    3126
Asn Thr Leu Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly
            220             225             230

gtc tat ttt tgt gca agc ctt tac ttc ggc ttc ccc tgg ttt gct tat    3174
Val Tyr Phe Cys Ala Ser Leu Tyr Phe Gly Phe Pro Trp Phe Ala Tyr
            235             240             245

tgg ggc caa ggg acc ccg gtc acc gtc tcc agt gct aag ccc acc acg    3222
Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser Ala Lys Pro Thr Thr
250             255             260             265

acg cca gcg ccg cga cca cca aca ccg gcg ccc acc atc gcg tcg cag    3270
Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln
                270             275             280

ccc ctg tcc ctg cgc cca gag gcg gct cgg cca gcg gcg ggg ggc gca    3318
Pro Leu Ser Leu Arg Pro Glu Ala Ala Arg Pro Ala Ala Gly Gly Ala
            285             290             295

gtg cac acg agg ggg ctg gac ttc gcc ctg gat ccc aaa ctc tgc tac    3366
Val His Thr Arg Gly Leu Asp Phe Ala Leu Asp Pro Lys Leu Cys Tyr
            300             305             310
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ctg ctg gat gga atc ctc ttc atc tat ggt gtc att ctc act gcc ttg    3414
Leu Leu Asp Gly Ile Leu Phe Ile Tyr Gly Val Ile Leu Thr Ala Leu
        315             320             325

ttc ctg aga gtg aag ttc agc agg agc gca gag ccc ccc gcg tac cag    3462
Phe Leu Arg Val Lys Phe Ser Arg Ser Ala Glu Pro Pro Ala Tyr Gln
·330             335             340             345

cag ggc cag aac cag ctc tat aac gag ctc aat cta gga cga aga gag    3510
Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
            350             355             360

gag tac gat gtt ttg gac aag aga cgt ggc cgg gac cct gag atg ggg    3558
Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
        365             370             375

gga aag ccg aga agg aag aac cct cag gaa ggc ctg tac aat gaa ctg    3606
Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
        380             385             390

cag aaa gat aag atg gcg gag gcc tac agt gag att ggg atg aaa ggc    3654
Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
        395             400             405

gag cgc cgg agg ggc aag ggg cac gat ggc ctt tac cag ggt ctc agt    3702
·Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
410             415             420             425

aca gcc acc aag gac acc tac gac gcc ctt cac atg cag gcc ctg ccc    3750
Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
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cct cgc taa ctcgacgcgg ccgcggatcc ggattagtcc aatttgttaa    3799
Pro Arg
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atggaaaata cataactgag aatagagaag ttcagatcaa ggttaggaac agagagacag    4039

cagaatatgg gccaaacagg atatctgtgg taagcagttc ctgccccgct cagggccaag    4099

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            20                  25                  30


Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val
        35                  40                  45


Gly Thr Ser Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
    50                  55                  60


Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr Gly Val Pro Ser Arg
```

65   70   75   80

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser
                85   90   95

Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Leu
            100   105   110

Tyr Arg Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Gly Gly
            115   120   125

Ser Gly Ser Gly Gly Ser Gly Ser Gly Gly Ser Gly Ser Glu Val Gln
    130   135   140

Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg
145   150   155   160

Leu Ser Cys Ser Ala Ser Gly Phe Asp Phe Thr Thr Tyr Trp Met Ser
                165   170   175

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile Gly Glu Ile
            180   185   190

His Pro Asp Ser Ser Thr Ile Asn Tyr Ala Pro Ser Leu Lys Asp Arg
            195   200   205

Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Phe Leu Gln Met
    210   215   220

Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys Ala Ser Leu
225   230   235   240

Tyr Phe Gly Phe Pro Trp Phe Ala Tyr Trp Gly Gln Gly Thr Pro Val
            245   250   255

Thr Val Ser Ser Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro

           260   265   270

Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
        275   280   285

Ala Ala Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
    290   295   300

Phe Ala Leu Asp Pro Lys Leu Cys Tyr Leu Leu Asp Gly Ile Leu Phe
305   310   315   320

Ile Tyr Gly Val Ile Leu Thr Ala Leu Phe Leu Arg Val Lys Phe Ser
           325   330   335

Arg Ser Ala Glu Pro Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr
        340   345   350

Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys
      355   360   365

Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn
    370   375   380

Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu
385   390   395   400

Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly
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His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr
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Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
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region (aa20-138) with leader (aa1-19) (pertinent to Fig. 4A.)

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        1               5                   10

aca ggt gtc cac tcc gag gtc caa ctg gtg gag agc ggt gga ggt gtt           97
Thr Gly Val His Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val
15                  20                  25                  30

gtg caa cct ggc cgg tcc ctg cgc ctg tcc tgc tcc gca tct ggc ttc          145
Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe
                35                  40                  45

gat ttc acc aca tat tgg atg agt tgg gtg aga cag gca cct gga aaa          193
Asp Phe Thr Thr Tyr Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys
            50                  55                  60

ggt ctt gag tgg att gga gaa att cat cca gat agc agt acg att aac          241
Gly Leu Glu Trp Ile Gly Glu Ile His Pro Asp Ser Ser Thr Ile Asn
        65                  70                  75

tat gcg ccg tct cta aag gat aga ttt aca ata tcg cga gac aac gcc          289
Tyr Ala Pro Ser Leu Lys Asp Arg Phe Thr Ile Ser Arg Asp Asn Ala
    80                  85                  90

aag aac aca ttg ttc ctg caa atg gac agc ctg aga ccc gaa gac acc          337
Lys Asn Thr Leu Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr
95                  100                 105                 110

ggg gtc tat ttt tgt gca agc ctt tac ttc ggc ttc ccc tgg ttt gct          385
Gly Val Tyr Phe Cys Ala Ser Leu Tyr Phe Gly Phe Pro Trp Phe Ala
                115                 120                 125

tat tgg ggc caa ggg acc ccg gtc acc gtc tcc tca g                        422
Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser
            130                 135
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Val His Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln
            20   25   30

Pro Gly Arg Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Asp Phe
            35   40   45

Thr Thr Tyr Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
        50   55   60

Glu Trp Ile Gly Glu Ile His Pro Asp Ser Ser Thr Ile Asn Tyr Ala
65   70   75   80

Pro Ser Leu Lys Asp Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
                85   90   95

Thr Leu Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val
                100   105   110

Tyr Phe Cys Ala Ser Leu Tyr Phe Gly Phe Pro Trp Phe Ala Tyr Trp
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Gly Gln Gly Thr Pro Val Thr Val Ser Ser
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<223>  hMN14 VLCK, humanized (CDR-grafted) anti-CEA antibody kappa light
       chain V region (aa20-126), with human constant CK domain (aa127-
       232) and leader (aa1-19). (pertinent to Figure 4B.)


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           1               5                   10

aca gct aca ggt gtc cac tcc gac atc cag ctg acc cag agc cca agc       97
Thr Ala Thr Gly Val His Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser
        15                  20                  25

agc ctg agc gcc agc gtg ggt gac aga gtg acc atc acc tgt aag gcc      145
Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala
    30                  35                  40

agt cag gat gtg ggt act tct gta gct tgg tac cag cag aag cca ggt      193
Ser Gln Asp Val Gly Thr Ser Val Ala Trp Tyr Gln Gln Lys Pro Gly
45                  50                  55                  60

aag gct cca aag ctg ctg atc tac tgg aca tcc acc cgg cac act ggt      241
Lys Ala Pro Lys Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr Gly
                65                  70                  75

gtg cca agc aga ttc agc ggt agc ggt agc ggt acc gac ttc acc ttc      289
Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe
            80                  85                  90

acc atc agc agc ctc cag cca gag gac atc gcc acc tac tac tgc cag      337
Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln
        95                  100                 105

caa tat agc ctc tat cgg tcg ttc ggc caa ggg acc aag gtg gaa atc      385
Gln Tyr Ser Leu Tyr Arg Ser Phe Gly Gln Gly Thr Lys Val Glu Ile
    110                 115                 120

aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat      433
Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
125                 130                 135                 140

gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac      481
Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
```

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                     145                      150                      155
ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc      529
Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
            160                      165                      170

caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac agc aag gac      577
Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
            175                      180                      185

agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa gca gac tac      625
Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
    190                      195                      200

gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc      673
Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
205                      210                      215                  220

tcg ccc gtc aca aag agc ttc aac agg gga gag tgt taa                  712
Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                225                      230
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<212> PRT
<213> Homo sapiens and Mus sp.

<400> 6

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1               5                   10                  15

Val His Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala
            20                  25                  30

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val
        35                  40                  45

Gly Thr Ser Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
    50                  55                  60

Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr Gly Val Pro Ser Arg
65                  70                  75                  80
```

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser
                85   90   95

Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Leu
            100   105   110

Tyr Arg Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val
        115   120   125

Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys
    130   135   140

Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
145   150   155   160

Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
                165   170   175

Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
            180   185   190

Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
        195   200   205

Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
    210   215   220

Lys Ser Phe Asn Arg Gly Glu Cys
225   230